




(FILE 'HOME' ENTERED AT 17:51:03 ON 22 FEB 2005)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 17:51:05 ON 22 FEB 2005

L1	2192 S STREPTOMYCES (2N) AUREOFACIENS
L2	0 S L1 AND (HYDROXYBUTYRATE (3N) SYNTHASE)
L3	30 S L1 AND SYNTHASE
L4	12 DUP REM L3 (18 DUPLICATES REMOVED)
L5	12 S L1 AND (HYDROXYBUTYRATE OR PHB OR PHA OR POLYHYDROXYALKANOATE
L6	5 DUP REM L5 (7 DUPLICATES REMOVED)
L7	4 S NRRL2209
L8	2 DUP REM L7 (2 DUPLICATES REMOVED)

	Type	L #	Hits	Search Text
1	BRS	L1	2	"6756222"
2	BRS	L2	448	hydroxybutyrate and synthase
3	BRS	L3	34	l2 and aureofaciens
4	BRS	L4	40	hydroxybutyrate and aureofaciens
5	BRS	L5	10	phb and aureofaciens

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Range: from to Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD

☐ 1: [AAK53451](#). Reports putative PHA synt...[gi:25989121] BLink, Links

LOCUS AAK53451 813 aa linear BCT 13-APR-2004
 DEFINITION putative PHA synthase [Streptomyces aureofaciens].
 ACCESSION AAK53451
 VERSION AAK53451.1 GI:25989121
 DBSOURCE accession [AY032926.1](#)
 KEYWORDS .
 SOURCE Streptomyces aureofaciens
 ORGANISM [Streptomyces aureofaciens](#)
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptomycineae; Streptomycetaceae; Streptomyces.
 REFERENCE 1 (residues 1 to 813)
 AUTHORS Mahishi,L.H., Tripathi,G., Ramachander,T.V.N. and Rawal,S.K.
 TITLE Cloning, molecular analysis and heterologous expression of the
 poly(3-hydroxybutyrate) synthesizing genes from Streptomyces
 aureofaciens NRRL 2209
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 813)
 AUTHORS Mahishi,L.H., Tripathi,G., Ramachander,T.N. and Rawal,S.K.
 TITLE Direct Submission
 JOURNAL Submitted (21-APR-2001) Plant Tissue Culture Division, National
 Chemical Laboratory, Pashan Road, Pune, Maharashtra 411008, India
 COMMENT Method: conceptual translation supplied by author.
 FEATURES Location/Qualifiers
 source 1..813
 /organism="Streptomyces aureofaciens"
 /strain="NRRL 2209"
 /db_xref="taxon:1894"
 Protein 1..813
 /product="putative PHA synthase"
 /function="polymerization of hydroxyalkanoate monomers"
 CDS 1..813
 /gene="phaC"
 /coded_by="AY032926.1:2..2443"
 /transl_table=11

ORIGIN

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121 avldgaialw kgkagvrvt a cvggavmgfs almvglalsl tapgplgava pgvllltasa
181 aavagawrap kgfartggav aglaavaav gvpaaalpag wrvlayllcg laltavvrser
241 lpghaargvl aasgavvaga lvwalpp1aa vllgpvtvls dvwagtpdgf rsalgstlpw
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361 grgrcavarl vrlvrparcg grwsraafrg daargrrrgr ggarlggppa grraagrpr
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781 aspgrapvaw atqrarpsvr vgdgtgfept ssv

//

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[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

Database : A_Geneseq_16Dec04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
	No.	Score	Query Match	Length	DB	ID	
c	1	1267.5	14.5	19938	6	ABP76680	Abp76680 Streptomy
c	2	1132	12.9	19938	6	ABP76679	Abp76679 Streptomy
	3	1113.5	12.1	19938	6	ABP76679	Abp76679 Streptomy
c	4	1107.5	12.7	19938	6	ABP76682	Abp76682 Streptomy
	5	1081.5	11.7	1953	6	AAE36881	Aae36881 Nephila m
c	6	1075	12.3	19938	6	ABP76681	Abp76681 Streptomy
c	7	1018.5	11.6	2294	7	ABO68485	Abc68485 Pseudomon
c	8	1013	11.6	1706	7	ABO83014	Abc83014 Pseudomon
	9	996.5	10.8	19938	6	ABP76680	Abp76680 Streptomy
c	10	995	11.4	1071	7	ADF94310	Adf94310 Human col
c	11	980.5	11.2	1064	2	AAR93254	Aar93254 Collagen-
c	12	980.5	11.2	1064	2	AAW57652	Aaw57652 Collagen-
c	13	980.5	11.2	1065	2	AAR37741	Aar37741 Collagen-
c	14	970.5	11.1	19938	6	ABB98398	Abb98398 Streptomy
	15	958.5	10.4	19938	6	ABB98398	Abb98398 Streptomy
	16	913.5	9.9	19938	6	ABP76681	Abp76681 Streptomy

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	4824.4	100.0	4826	1	AY032926		AY032926 Streptomy
	3	1133	23.5	277000	1	SC0939109		AL939109 Streptomy
c	4	1096.4	22.7	299925	1	AP005048		AP005048 Streptomy
c	5	528	10.9	302007	1	SC0939132		AL939132 Streptomy
c	6	331.8	6.9	3030	8	VCA429230		AJ429230 Volvox ca
	7	314.4	6.5	167254	9	CNS05TDS		AL357093 Human chr
c	8	282.6	5.9	110000	1	AE000516_27		Continuation (28 o
c	9	282.6	5.9	346051	1	BX842580		BX842580 Mycobacte

12: geneseqn2004as:*

13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
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	2	4822.8	99.9	4826	8	ABX93509			Abx93509 DNA fragm
	3	294.4	6.1	114955	2	AAX53491			Aax53491 Human ade
c	4	282.6	5.9	110000	4	AAI99682_27			Continuation (28 o
c	5	282.6	5.9	110000	4	AAI99682_28			Continuation (29 o
c	6	282.6	5.9	110000	4	AAI99683_27			Continuation (28 o
c	7	271.8	5.6	114955	2	AAX53491			Aax53491 Human ade
	8	262.6	5.4	110000	4	AAI99683_39			Continuation (40 o
	9	260.4	5.4	110000	4	AAI99682_39			Continuation (40 o
c	10	257.4	5.3	2543	12	ACH87341			Ach87341 Human gen
c	11	257	5.3	110000	4	AAI99683_06			Continuation (7 of
	12	255.4	5.3	3921	8	ACA40351			Aca40351 Prokaryot
c	13	255.4	5.3	110000	4	AAI99682_06			Continuation (7 of
c	14	253	5.2	110000	4	AAI99683_39			Continuation (40 o
c	15	242.2	5.0	110000	4	AAI99682_39			Continuation (40 o
c	16	241.2	5.0	110000	4	AAI99682_37			Continuation (38 o
	17	239.6	5.0	110000	4	AAI99682_12			Continuation (13 o

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Query					
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c	2	282.6	5.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	3	282.6	5.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	4	262.6	5.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	5	260.4	5.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	6	188.2	3.9	6192	2	US-08-479-537A-1	Sequence 1, Appli
c	7	188.2	3.9	6192	3	US-09-083-116-1	Sequence 1, Appli
c	8	188.2	3.9	6192	3	US-09-134-916A-1	Sequence 1, Appli
c	9	188.2	3.9	6449	2	US-08-479-537A-4	Sequence 4, Appli
c	10	188.2	3.9	6449	3	US-09-083-116-4	Sequence 4, Appli
c	11	188.2	3.9	6449	3	US-09-134-916A-4	Sequence 4, Appli
	12	188	3.9	2457	4	US-09-863-859-21	Sequence 21, Appl
	13	188	3.9	4881	4	US-09-863-859-23	Sequence 23, Appl
	14	180	3.7	8438	1	US-07-945-283-1	Sequence 1, Appli

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hlc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query					Description
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c	2	275.6	5.7	1695	8	CC290874	CC290874 CH261-172
c	3	266.6	5.5	1674	9	CL078342	CL078342 CH216-149
c	4	263.4	5.5	2332	9	AG363333	AG363333 Mus muscu
	5	262.2	5.4	1956	9	CG754548	CG754548 P050-1-A1
	6	261.6	5.4	1909	9	CL078604	CL078604 CH216-151
	7	259.4	5.4	1628	9	CG757066	CG757066 P052-2-A0
	8	258.2	5.4	1970	9	CG748837	CG748837 P042-4-E0
	9	253	5.2	1738	9	CG750956	CG750956 P045-2-H0
c	10	251.6	5.2	2198	9	AG332729	AG332729 Mus muscu
	11	251	5.2	1839	9	CG747711	CG747711 P041-2-E0
c	12	248.4	5.1	1788	8	CC320563	CC320563 TAM32-34P
	13	247.4	5.1	1793	9	CG754612	CG754612 P050-1-D0

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 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%							
Result			Query						
No.	Score	Match	Length	DB	ID			Description	
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c	2	841	9.6	924	2	S27923		gene LF3 protein -	
	3	829	9.0	1660	2	A70869		hypothetical glyci	
c	4	822	9.4	4776	2	E95206		cell wall surface	
	5	800	8.7	1489	2	D70807		hypothetical glyci	
	6	795	8.6	2639	2	T31328		fibroin - Chinese	
	7	791.5	8.6	1381	2	E70806		hypothetical glyci	
	8	791	8.6	1901	2	F70806		hypothetical glyci	
	9	781.5	8.5	1079	2	B70807		hypothetical glyci	
	10	777.5	8.4	1306	2	A70934		hypothetical glyci	
	11	776.5	8.4	1329	2	E70917		hypothetical glyci	
c	12	776.5	8.9	1344	1	A35175		mucin 1 precursor,	
	13	775	8.4	1466	1	CGHU7L		collagen alpha 1(I	
	14	774.5	8.4	13288	2	T03099		mucin, submaxillar	
	15	753	8.2	2944	2	A54849		collagen alpha 1(V	

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 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	3	1795	19.5	368	2	Q8GFF1	Q8gff1 streptomyce
	4	1629	17.7	796	2	Q827V3	Q827v3 streptomyce
	5	1509	16.4	818	2	Q9F3E4	Q9f3e4 streptomyce
c	6	1351	15.4	263	2	Q8GFE8	Q8gfe8 streptomyce
c	7	1255	14.3	245	2	Q8GFF0	Q8gff0 streptomyce
c	8	1133.5	13.0	3409	2	Q6SSE6	Q6sse6 chlamydomon
c	9	1109.5	12.7	3889	2	Q6SSE8	Q6sse8 chlamydomon
	10	1081.5	11.7	1953	2	Q9BIT7	Q9bit7 nephila ina
c	11	1057.5	12.1	676	2	Q95JC9	Q95jc9 sus scrofa
c	12	1020	11.7	190	2	Q8GFE9	Q8gfe9 streptomyce
	13	930.5	10.1	1884	2	Q9NHW2	Q9nhw2 nephila ina
c	14	914.5	10.5	7524	2	Q6PZE0	Q6pze0 mus musculu
	15	891.5	9.7	2249	2	Q9NHW4	Q9nhw4 nephila cla
c	16	891	10.2	566	2	Q95JD1	Q95jd1 sus scrofa
c	17	863.5	9.9	1188	2	Q41805	Q41805 zea mays (m
c	18	841.5	9.6	2752	2	Q9UQ35	Q9uq35 homo sapien